

SEQUENCE LISTING

<110> Hoechst Marion Roussel

<120> Novel monomer protein with bone morphogenetic activity
and medicinal agent containing the same for preventing
and treating diseases of cartilage and bone.

<130> JH98K008 PCT SEQUENCES IN ENGLISH

<140>

<141>

<150> 10-141379

<151> 1998-05-22

<160> 4

<170> PatentIn Ver. 2.1

<210> 1

<211> 357

<212> DNA

<213> HUMAN

<220>

<221> CDS

<222> (1)..(357)

<223> Relevant amino acid residues in SEQ ID NO 1 from 1
to 82 and from 84 to 119 in WO 95/04819.

Note : aminoacid residue 83 is alanine
instead of cysteine.

<300>

<301> HOTTEN, Gertrud

NEIDHARDT, Helge

PAULISTA, Michael

<302> New growth/differentiation factor of the tgf-beta
familie.

<310> WO 95/04819

<311> 1995-02-16

<400> 1

cca cta gca act cgt cag ggc aag cga ccc agc aag aac ctt aag gct	48
Pro Leu Ala Thr Arg Gln Gly Lys Arg Pro Ser Lys Asn Leu Lys Ala	
1 5 10 15	
cgc tgc agt cgg aag gca ctg cat gtc aac ttc aag gac atg ggc tgg	96
Arg Cys Ser Arg Lys Ala Leu His Val Asn Phe Lys Asp Met Gly Trp	
20 25 30	
gac gac tgg atc atc gca ccc ctt gag tac gag gct ttc cac tgc gag	144
Asp Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu	
35 40 45	
ggg ctg tgc gag ttc cca ttg cgc tcc cac ctg gag ccc acg aat cat	192
Gly Leu Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His	
50 55 60	
gca gtc atc cag acc ctg atg aac tcc atg gac ccc gag tcc aca cca	240
Ala Val Ile Gln Thr Leu Met Asn Ser Met Asp Pro Glu Ser Thr Pro	
65 70 75 80	
ccc acc gcc tgt gtg ccc acg cga ctg agt ccc atc agc atc ctc ttc	288
Pro Thr Ala Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe	
85 90 95	
att gac tct gcc aac aac gtg gtg tat aag cag tat gag gac atg gtc	336
Ile Asp Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val	
100 105 110	
gtg gag tcg tgt ggc tgt agg	357
Val Glu Ser Cys Gly Cys Arg	
115	

<210> 2

<211> 119

<212> PRT

<213> HUMAN

<400> 2

Pro Leu Ala Thr Arg Gln Gly Lys Arg Pro Ser Lys Asn Leu Lys Ala

1

5

10

15

Arg Cys Ser Arg Lys Ala Leu His Val Asn Phe Lys Asp Met Gly Trp

20

25

30

Asp Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu

35

40

45

Gly Leu Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His

50

55

60

Ala Val Ile Gln Thr Leu Met Asn Ser Met Asp Pro Glu Ser Thr Pro

65

70

75

80

Pro Thr Ala Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe

85

90

95

Ile Asp Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val

100

105

110

Val Glu Ser Cys Gly Cys Arg

115

<210> 3

<211> 39

<212> DNA

<213> HUMAN

<220>

<221> misc_feature

<222> (1)..(39)

<223> Sense PCR primer for mutation introducing.

<400> 3

catgccatgg accccgagtc cacaccaccc accgcctgt

39

<210> 4

<211> 37

<212> DNA

<213> HUMAN

<220>

<221> misc_feature

<222> Complement((1)..(37))

<223> Reverse PCR primer for mutation introducing.

<400> 4

cccaagcttg catgcctgcc ggtcgactac ctacagc

37